

USING A BLIND PREDICTION PROCESS TO TEST THE METHODS OF PREDICTING STRUCTURE FROM SEQUENCE

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Predicting protein structure from sequence remains a difficult problem. To effectively advance the methodology an objective process of the method assessment is necessary. A center dedicated to support such a process has recently been created. The Livermore based facility provides prediction targets, accepts predictions, and makes evaluations according to a detailed set of criteria. Targets for predictions are selected from structures that are about to be released publicly. Predictions are accepted in comparative modeling, fold recognition, and ab initio folding. The center provides this service on continuing basis as well as in conjunction with the bi-annual Meeting on Critical Assessment of Techniques for Protein Structure Prediction (CASP1 1994 and CASP2 1996). The details of the blind prediction process, evaluation criteria, and the operation of the center will be presented.

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